OIPE

RAW SEQUENCE LISTING DATE: 08/28/2001 PATENT APPLICATION: US/09/837,235 TIME: 10:22:38

Input Set : A:\9725-005-999.txt.

Output Set: N:\CRF3\08282001\1837235.raw

```
5 <110> APPLICANT: Marshall, Christopher
 7
         Hoffman, Alexander
                                                             ENTERED
 9
         Errico, Joseph
11
         Marshall, Paul
15 <120> TITLE OF INVENTION: STABILIZED PROTEINS
19 <130> FILE REFERENCE: 9725-005-999
23 <140> CURRENT APPLICATION NUMBER: 09/837,235
25 <141> CURRENT FILING DATE: 2001-04-18
29 <150> PRIOR APPLICATION NUMBER: PCT/US00/28595
31 <151> PRIOR FILING DATE: 2000-10-16
35 <150> PRIOR APPLICATION NUMBER: 60/159,763
37 <151> PRIOR FILING DATE: 1999-10-15
41 <160> NUMBER OF SEQ ID NOS: 42
45 <170> SOFTWARE: PatentIn version 3.0
49 <210> SEQ ID NO: 1
51 <211> LENGTH: 954
53 <212> TYPE: DNA
55 <213> ORGANISM: Candida antarctica
59 <400> SEOUENCE: 1
60 ctacetteeg gtteggaeee tgeetttteg cageecaagt eggtgetega tgegggtetg
                                                                          60
62 acctgccagg gtgcttcgcc atcctcggtc tccaaaccca tccttctcgt ccccggaacc
                                                                         120
64 ggcaccacag gtccacagtc gttcgactcg aactggatcc ccctctcaac gcagttgggt
                                                                         180
66 tacacaccet getggatete acceeegeeg tteatgetea aegacaceca ggteaacaeg
                                                                         240
68 gagtacatgg tcaacgccat caccgcgctc tacgctggtt cgggcaacaa caagcttccc
                                                                         300
70 gtgcttacct ggtcccaggg tggtctggtt gcacagtggg gtctgacctt cttccccagt
                                                                         360
72 atcaggtcca aggtcgatcg acttatggcc tttgcgcccg actacaaggg caccgtcctc
                                                                         420
74 geoggeeete tegatgeaet egeggttagt geacceteeg tatggeagea aaccaeeggt
                                                                         480
                                                                         540
76 teggeactea ceacegeact eegaaaegea ggtggtetga eecagategt geecaceace
78 aacctetact eggegaeega egagategtt eageeteagg tgteeaacte geeactegae
                                                                         600
80 teatectace tetteaacgg aaagaacgte caggeacagg cegtgtgtgg geegetgtte
                                                                         660
82 gtcatcgace atgcaggete geteaceteg cagttetect acgtcgtegg tegateegee
                                                                         720
                                                                         780
84 ctgcgctcca ccacgggcca ggctcgtagt gcagactatg gcattacgga ctgcaaccct
86 cttcccgcca atgatetgae teccgageaa aaggtegeeg eggetgeget eetggegeeg
                                                                         840
                                                                         900
88 gcagctgcag ccatcgtggc gggtccaaag cagaactgcg agcccgacct catgccctac
90 geocgecet ttgcagtagg caaaaggace tgctccggca tcgtcaccce ctga
                                                                         954
93 <210> SEQ ID NO: 2
95 <211> LENGTH: 317
97 <212> TYPE: PRT
99 <213> ORGANISM: Candida antarctica
103 <400> SEQUENCE: 2
105 Leu Pro Ser Gly Ser Asp Pro Ala Phe Ser Gln Pro Lys Ser Val Leu
106 1
                                        10
108 Asp Ala Gly Leu Thr Cys Gln Gly Ala Ser Pro Ser Ser Val Ser Lys
109
111 Pro Ile Leu Leu Val Pro Gly Thr Gly Thr Gly Pro Gln Ser Phe
112
114 Asp Ser Asn Trp Ile Pro Leu Ser Thr Gln Leu Gly Tyr Thr Pro Cys
```

DATE: 08/28/2001 TIME: 10:22:38 RAW SEQUENCE LISTING PATENT APPLICATION: US/09/837,235

Input Set : A:\9725-005-999.txt
Output Set: N:\CRF3\08282001\I837235.raw

		~ ^															
115		50					55		_	_	_	60			_	_,	
	Trp	Ile	Ser	Pro	Pro		Phe	Met	Leu	Asn		Thr	GIn	vaı	Asn		
118						70	_		_		75	_		_		80	
	Glu	Tyr	Met	Val		Ala	Ile	Thr	Ala		Tyr	Ala	Gly	Ser		Asn	
121					85					90					95		
123	Asn	Lys	Leu		Val	Leu	Thr	Trp		Gln	Gly	Gly	Leu	Val	Ala	Gln	
124				100					105					110			
126	${\tt Trp}$	Gly		Thr	Phe	Phe	Pro		Ile	Arg	Ser	Lys	Val	Asp	Arg	Leu	
127			115					120					125				
129	Met	Ala	Phe	Ala	Pro	Asp		Lys	Gly	Thr	Val	Leu	Ala	Gly	Pro	Leu	
130		130					135					140					
132	Asp	Ala	Leu	Ala	Val	Ser	Ala	Pro	Ser	Val	_		Gln	Thr	Thr	Gly	
	145					150					155				•	160	
135	Ser	Ala	Leu	Thr	Thr	Ala	Leu	Arg	Asn	Ala	Gly	Gly	Leu	Thr	Gln	Ile	
136					165					170					175		
138	Val	Pro	Thr	Thr	Asn	Leu	Tyr	Ser	Ala	Thr	Asp	Glu	Ile	Val	Gln	Pro	
139				180			*		185					190			
141	Gln	Val	Ser	Asn	Ser	Pro	Leu	Asp	Ser	Ser	Tyr	Leu	Phe	Asn	Gly	Lys	
142			195					200					205				
144	Asn	Val	Gln	Ala	${\tt Gln}$	Ala	Val	Cys	Gly	Pro	Leu	Phe	Val	Ile	Asp	His	
145		210					215					220					
147	Ala	Gly	Ser	Leu	Thr	Ser	${\tt Gln}$	Phe	Ser	Tyr	Val	Val	Gly	Arg	Ser	Ala	
148	225					230					235					240	
150	Leu	Arg	Ser	Thr	Thr	Gly	Gln	Ala	Arg	Ser	Ala	Asp	Tyr	Gly	Ile	Thr	
151					245					250					255		
153	Asp	Cys	Asn	Pro	Leu	Pro	Ala	Asn	Asp	Leu	Thr	Pro	Glu	Gln	Lys	Val	
154				260					265					270			
156	Ala	Ala	Ala	Ala	Leu	Leu	Ala	Pro	Ala	Ala	Ala	Ala	Ile	Val	Ala	Gly	
157			275					280					285				
159	Pro	Lys	Gln	Asn	Cys	Glu	Pro	Asp	Leu	Met	Pro	Tyr	Ala	Arg	Pro	Phe	
160		290					295					300					
162	Ala	Val	Gly	Lys	Arg	Thr	Cys	Ser	Gly	Ile	Val	Thr	Pro				
163	305					310					315						
165	<210)> SI	EQ II	ON C	: 3												
167	<211	L> LI	ENGTI	H: 57	7												
169	<212	2> T	PE:	DŅA													
171	<213	3> OI	RGANI	ISM:	Cano	lida	anta	arct	ica								
175	<400)> SI	EQUE	NCE:	3												
176	atgg	gaat	tc d	catca	itcat	c at	cato	cacaç	j cag	gegge	cta	ccti	tccg	gtt (eggad	ccc	57
179	<210)> SI	EQ II	ON C	4												
181	<211	L> LI	ENGTI	H: 37	7												
183	<212	2> T	PE:	DNA													
185	<213	3> OI	RGAN	ISM:	Cano	lida	anta	rcti	ca								
189	<400)> SI	EQUE	ICE:	4												
	ctct					a go	rgggt	gac	, ato	geegg	Ŧ						37
	<210																
195	<211	L> LE	ENGTE	i: 68	3												
197	<212	2> TY	PE:	DNA													
199	<213	3> OF	RGANI	SM:	Cand	lida	anta	rcti	ca								

DATE: 08/28/2001 TIME: 10:22:38 RAW SEQUENCE LISTING PATENT APPLICATION: US/09/837,235

Input Set : A:\9725-005-999.txt
Output Set: N:\CRF3\08282001\1837235.raw

	·	
203	<400> SEQUENCE: 5	
204	atgggaatte cateateate ateateaeag eageggeeta eetteeggtt eggaeeetge	60
206	ctattcgc	68
209	<210> SEQ ID NO: 6	
211	<211> LENGTH: 24	
213	<212> TYPE: DNA	
215	<213> ORGANISM: Candida antarctica	
219	<400> SEQUENCE: 6	
220	cgactcgaac tacatccccc tctc	24
	<210> SEQ ID NO: 7	
225	<211> LENGTH: 24	
	<212> TYPE: DNA	
	<213> ORGANISM: Candida antarctica	
-	<400> SEQUENCE: 7	
	gagaggggga tgtagttcga gtcg	24
	<210> SEQ ID NO: 8	
	<211> LENGTH: 25	
	<212> TYPE: DNA	
	<213> ORGANISM: Candida antarctica	
	<400> SEQUENCE: 8	
	gggtctgacc tacttcccca gtatc	25
	<210> SEQ ID NO: 9	
	<211> LENGTH: 25	
	<212> TYPE: DNA	
	<213> ORGANISM: Candida antarctica	
	<400> SEQUENCE: 9	
	gatactgggg aagtaggtca gaccc	25
	<210> SEQ ID NO: 10	
	<211> LENGTH: 21	
	<212> TYPE: DNA	
	<213> ORGANISM: Candida antarctica	
	<400> SEQUENCE: 10	
	cgatgagatt tccttcaatt t	21
	<210> SEQ ID NO: 11	
	<211> LENGTH: 21	
	<212> TYPE: DNA	
	<213> ORGANISM: Candida antarctica	
	<400> SEQUENCE: 11	
	tctagaaagg tggcggccgc c	21
	<210> SEQ ID NO: 12	
	<211> LENGTH: 22	
	<212> TYPE: DNA	
	<213> ORGANISM: Candida antarctica	
	<400> SEQUENCE: 12	
	gaagetggat tecateatea te	22
	<210> SEQ ID NO: 13	
	<211> LENGTH: 21	
	<212> TYPE: DNA	
	<213> ORGANISM: Candida antarctica	
713	. Canada antaretica	

RAW SEQUENCE LISTING DATE: 08/28/2001 PATENT APPLICATION: US/09/837,235 TIME: 10:22:38

Input Set : A:\9725-005-999.txt

Output Set: N:\CRF3\08282001\I837235.raw

317	<400)> S	EQUE	NCE:	13					•							
318	tcta	igaa	agg '	tggc	ggcc	gc c											21
321	<210)> S	EQ I	D NO	: 14												
323	<211	L> L	ENGT	H: 10	074												
325	<212	2> T	YPE:	DNA													
327	<213	3> 0	RGAN:	ISM:	Bac	illu	s sul	otil:	is								
331	<400)> S	EQUE	NCE:	14												
332	atgt	ctg	tgc a	aggct	tgcc	gg a	aaaa	gcagi	ac	agaaa	aaga	aata	acati	tgt	cggat	tttaaa	60
334	caga	caa	tga 🤄	gtgc	catga	ag ti	tccg	ccaa	g aa	aaag	gatg	tta	tttc	tga	aaaa	ggcgga	120
336	aagg	jttc	aaa a	agcaa	attta	aa g	tatg	taad	g gc	ggcc	gcag	caa	catte	gga	tgaaa	aaagct	180
338	gtaa	aag	aat 1	tgaaa	aaaa	ga to	ccga	gcgti	ge	atat	gtgg	aaga	aagat	tca	tatte	gcacat	240
340	gaat	atg	ege a	aatct	tgtto	cc ti	tatg	gcati	tc.	tcaaa	atta	aage	egee	ggc	tctt	cactct	300
342	caag	gct	aca (caggo	ctcta	aa c	gtaa	aagta	a gc	tgtta	atcg	aca	gegga	aat	tgact	tcttct	360
344	cato	ctg	act 1	taaa	cgtca	ag ag	ggcg	gagca	a ago	cttc	gtac	ctt	ctgaa	aac	aaac	ccatac	420
346	cagg	gacg	gca	gttci	tcac	gg ta	acgc	atgta	a gc	cggta	acga	ttg	ceget	tct	taata	aactca	480
348	atcg	gtg	ttc 1	tgggd	cgtta	ag co	ccaa	gegea	a tca	attai	tatg	cagi	taaaa	agt	gctt	gattca	540
350	acag	gaa	gcg (gccaa	atata	ag ci	tggai	tati	aa	egge	attg	agt	gggc	cat	ttcca	aacaat	600
352	atgg	gatg	tta 1	tcaad	catga	ag co	cttg	gegga	a cc	tact	ggtt	ctac	cago	gct	gaaaa	acagtc	660
354	gttg	jaca	aag (ccgti	ttcca	ag c	ggtai	cgt	gti	tgct	gccg	cago	ccgga	aaa	cgaa	ggttca	720
356	tccg	gaa	gca (caago	caca	jt c	ggcta	accct	ge	aaaa	tatc	ctt	ctact	tat	tgcag	gtaggt	780
358	gcgg	rtaa	aca q	gcago	caac	ca aa	agago	cttca	a tto	ctcca	agcg	cago	gttci	tga	gctt	gatgtg	840
360	atgg	jctc	ctg	gegt	gtcca	at co	caaa	gcaca	a ct	tcct	ggag	gcad	cttac	cgg	cgcti	tataac	900
362	ggaa	cgt	cca 1	tggc	gacto	cc to	cacgi	tgc	gga	agcag	gcag	cgti	caati	tct	ttcta	aagcac	960
																cttgga	
200												~~~					4054
300	aact	CLL	tct a	actat	tggaa	aa ag	gggti	caato	c aac	cgtac	caag	cage	ctgca	aca	ataa		1074
	<210					aa aq	gggti	caato	c aa	gtad	caag	cayo	ctgca	aca	ataa		10/4
369)> S	EQ II	ON C	: 15	aa aq	gggti	caato	c aa	gtae	caag	cayo	ctgca	aca	ataa		10/4
369 371	<210)> Si .> Li	EQ II ENGTI	O NO:	: 15	aa a	gggti	laato	c aa	gtao ,	caag	cago	etgea	aca	ataa		1074
369 371 373	<210 <211)> S1 .> L1 !> T1	EQ II ENGTI YPE:	O NO: H: 35 PRT	: 15 57					gtac	caag	cago	etge	aca	ataa		1074
369 371 373 375 379	<210 <211 <212 <213 <400)> S1 .> L1 ?> T1 3> O1)> S1	EQ II ENGTI YPE: RGANI EQUEI	O NO: H: 35 PRT ISM: NCE:	: 15 57 Baci 15	illus	s sul	o til i	is	,							1074
369 371 373 375 379 381	<210 <211 <212 <213 <400 Met)> S1 .> L1 ?> T1 3> O1)> S1	EQ II ENGTI YPE: RGANI EQUEI	O NO: H: 35 PRT ISM: NCE:	: 15 57 Baci 15	illus	s sul	o til i	is	Ser					Tyr	Ile	1074
369 371 373 375 379 381 382	<210 <211 <212 <213 <400 Met 1)> S) .> L) ?> T) 3> O) > S) Ser	EQ II ENGTI YPE: RGANI EQUEI Val	NO: H: 35 PRT ISM: NCE: Gln	: 15 57 Baci 15 Ala 5	illus Ala	s sul Gly	tili Lys	ls Ser	Ser 10	Thr	Glu	Lys	Lys	Tyr 15		1074
369 371 373 375 379 381 382 384	<210 <211 <212 <213 <400 Met)> S) .> L) ?> T) 3> O) > S) Ser	EQ II ENGTI YPE: RGANI EQUEI Val	NO: H: 35 PRT ISM: NCE: Gln	: 15 57 Baci 15 Ala 5	illus Ala	s sul Gly	tili Lys	is Ser Ala	Ser 10	Thr	Glu	Lys	Lys Lys	Tyr 15		1074
369 371 373 375 379 381 382 384 385	<210 <211 <212 <213 <400 Met 1 Val)> S) > L) > T' S> O) S> S) Ser Gly	EQ II ENGTI YPE: RGAN: EQUEI Val Phe	PRT ISM: NCE: Gln Lys	: 15 57 Baci 15 Ala 5 Gln	illus Ala Thr	s sul Gly Met	tili Lys Ser	ser Ala 25	Ser 10 Met	Thr	Glu Ser	Lys Ala	Lys Lys 30	Tyr 15 Lys	Lys	1074
369 371 373 375 379 381 382 384 385 387	<210 <211 <212 <213 <400 Met 1)> S) > L) > T' S> O) S> S) Ser Gly	EQ II ENGTI YPE: RGANI EQUEI Val Phe	PRT ISM: NCE: Gln Lys	: 15 57 Baci 15 Ala 5 Gln	illus Ala Thr	s sul Gly Met	Lys Ser Gly	ser Ala 25	Ser 10 Met	Thr	Glu Ser	Lys Ala Gln	Lys Lys 30	Tyr 15 Lys	Lys	1074
369 371 373 375 379 381 382 384 385 387 388	<210 <211 <212 <213 <400 Met 1 Val)> S) > L) > T) 3> O) > S) Ser Gly Val	EQ II ENGTI YPE: RGANI EQUEI Val Phe Ile 35	D NO: H: 35 PRT ISM: NCE: Gln Lys 20 Ser	Baci 15 Ala 5 Gln	illus Ala Thr Lys	S sub Gly Met Gly	Lys Ser Gly	s Ser Ala 25 Lys	Ser 10 Met	Thr Ser Gln	Glu Ser Lys	Lys Ala Gln 45	Lys Lys 30 Phe	Tyr 15 Lys	Lys Tyr	1074
369 371 373 375 379 381 382 384 385 387 388	<210 <211 <212 <213 <400 Met 1 Val)> Si > Li > Ti 3> Oi > Si Ser Gly Val	EQ II ENGTI YPE: RGANI EQUEI Val Phe Ile 35	D NO: H: 35 PRT ISM: NCE: Gln Lys 20 Ser	Baci 15 Ala 5 Gln	illus Ala Thr Lys	S sub Gly Met Gly Thr	Lys Ser Gly	s Ser Ala 25 Lys	Ser 10 Met	Thr Ser Gln	Glu Ser Lys Ala	Lys Ala Gln 45	Lys Lys 30 Phe	Tyr 15 Lys	Lys Tyr	1074
369 371 373 375 381 382 384 385 387 388 390 391	<210 <211 <212 <213 <400 Met 1 Val Asp	0> S1 2> L1 2> T3 3> O1 0> S1 Ser Gly Val Asn 50	EQ II ENGTI YPE: RGANI EQUEI Val Phe Ile 35 Ala	D NO: H: 35 PRT ISM: NCE: Gln Lys 20 Ser	Bacca 15 Ala 5 Gln Glu	illus Ala Thr Lys Ala	Gly Met Gly Thr	Lys Ser Gly 40 Leu	Ser Ala 25 Lys Asp	Ser 10 Met Val Glu	Thr Ser Gln Lys	Glu Ser Lys Ala 60	Lys Ala Gln 45 Val	Lys Lys 30 Phe Lys	Tyr 15 Lys Lys Glu	Lys Tyr Leu	1074
369 371 373 375 381 382 384 385 387 388 390 391 393	<210 <211 <212 <213 <400 Met 1 Val Asp Val Lys	0> Si 2> Li 2> Ti 3> Oi 0> Si Ser Gly Val Asn 50 Lys	EQ II ENGTI YPE: RGAN: EQUEI Val Phe Ile: 35 Ala	D NO: H: 35 PRT ISM: NCE: Gln Lys 20 Ser Ala Pro	Baci 15 Ala 5 Gln Glu Ala Ser	Ala Thr Lys Ala Val	Gly Met Gly Thr 55 Ala	Lys Ser Gly 40 Leu	ser Ala 25 Lys Asp	Ser 10 Met Val Glu	Thr Ser Gln Lys Glu	Glu Ser Lys Ala 60 Asp	Lys Ala Gln 45 Val	Lys Lys 30 Phe Lys	Tyr 15 Lys Lys Glu	Lys Tyr Leu His	1074
369 371 373 375 381 382 384 385 387 388 390 391 393 394	<210 <211 <212 <213 <400 Met 1 Val Asp Val Lys 65	O> SI > LI > TY S> OI O> SI Ser Gly Val Asn 50 Lys	EQ II ENGTI YPE: RGAN: EQUE Val Phe Ile 35 Ala Asp	D NO: H: 35 PRT ISM: NCE: Gln Lys 20 Ser Ala Pro	Baci 15 Ala 5 Gln Glu Ala Ser	Ala Thr Lys Ala Val 70	Gly Met Gly Thr 55 Ala	Lys Ser Gly 40 Leu	Ser Ala 25 Lys Asp	Ser 10 Met Val Glu	Thr Ser Gln Lys Glu 75	Glu Ser Lys Ala 60 Asp	Lys Ala Gln 45 Val	Lys Lys 30 Phe Lys	Tyr 15 Lys Lys Glu Ala	Lys Tyr Leu His	1074
369 371 373 375 381 382 384 385 387 388 390 391 393 394 396	<210 <211 <212 <213 <400 Met 1 Val Asp Val Lys	O> SI > LI > TY S> OI O> SI Ser Gly Val Asn 50 Lys	EQ II ENGTI YPE: RGAN: EQUE Val Phe Ile 35 Ala Asp	D NO: H: 35 PRT ISM: NCE: Gln Lys 20 Ser Ala Pro	Baci 15 Ala 5 Gln Glu Ala Ser	Ala Thr Lys Ala Val 70	Gly Met Gly Thr 55 Ala	Lys Ser Gly 40 Leu	Ser Ala 25 Lys Asp	Ser 10 Met Val Glu Glu	Thr Ser Gln Lys Glu 75	Glu Ser Lys Ala 60 Asp	Lys Ala Gln 45 Val	Lys Lys 30 Phe Lys	Tyr 15 Lys Lys Glu Ala Ala	Lys Tyr Leu His	1074
369 371 373 375 381 382 384 385 387 388 390 391 393 394 396 397	<210 <211 <212 <213 <400 Met 1 Val Asp Val Lys 65 Glu	O> SI > LI P> TY S> OI O> SI Ser Gly Val Asn 50 Lys	EQ II ENGTI YPE: RGANI EQUEI Val Phe Ile 35 Ala Asp Ala	D NO: H: 35 PRT ISM: NCE: Gln Lys 20 Ser Ala Pro Gln	Bace 15 Ala 5 Gln Glu Ala Ser 85	Ala Thr Lys Ala Val 70 Val	Gly Met Gly Thr 55 Ala	Lys Ser Gly 40 Leu Tyr	Ser Ala 25 Lys Asp Val Gly	Ser 10 Met Val Glu Glu Ile 90	Thr Ser Gln Lys Glu 75 Ser	Glu Ser Lys Ala 60 Asp	Lys Ala Gln 45 Val His	Lys Lys 30 Phe Lys Ile Lys	Tyr 15 Lys Lys Glu Ala Ala 95	Lys Tyr Leu His 80 Pro	1074
369 371 373 375 381 382 384 385 387 388 391 393 394 396 397 399	<210 <211 <212 <213 <400 Met 1 Val Asp Val Lys 65	O> SI > LI P> TY S> OI O> SI Ser Gly Val Asn 50 Lys	EQ II ENGTI YPE: RGANI EQUEI Val Phe Ile 35 Ala Asp Ala	PRT ISM: ISM: ICE: Gln Lys 20 Ser Ala Pro Gln Ser	Bace 15 Ala 5 Gln Glu Ala Ser 85	Ala Thr Lys Ala Val 70 Val	Gly Met Gly Thr 55 Ala	Lys Ser Gly 40 Leu Tyr	Ser Ala 25 Lys Asp Val Gly	Ser 10 Met Val Glu Glu Ile 90	Thr Ser Gln Lys Glu 75 Ser	Glu Ser Lys Ala 60 Asp	Lys Ala Gln 45 Val His	Lys Lys 30 Phe Lys Ile Lys Val	Tyr 15 Lys Lys Glu Ala Ala 95	Lys Tyr Leu His 80 Pro	1074
369 371 373 375 381 382 384 385 387 388 391 393 394 396 397 399 400	<210 <211 <212 <213 <400 Met 1 Val Asp Val Lys 65 Glu Ala	> Si > Li > Ti > Oi > Si Ser Gly Val Asn 50 Lys Tyr	EQ II ENGTI YPE: RGANT EQUE Val Phe Ile 35 Ala Asp Ala His	PRT ISM: ISM: ICE: Gln Lys 20 Ser Ala Pro Gln Ser 100	Bacs 15 Ala 5 Glu Ala Ser Ser 85 Gln	Ala Thr Lys Ala Val 70 Val Gly	Gly Met Gly Thr 55 Ala Pro	Lys Ser Gly 40 Leu Tyr Tyr	Ser Ala 25 Lys Asp Val Gly Gly 105	Ser 10 Met Val Glu Glu Ile 90 Ser	Thr Ser Gln Lys Glu 75 Ser Asn	Glu Ser Lys Ala 60 Asp Gln Val	Lys Ala Gln 45 Val His Ile	Lys Lys 30 Phe Lys Ile Lys Val 110	Tyr 15 Lys Glu Ala Ala 95 Ala	Lys Tyr Leu His 80 Pro	1074
369 371 373 375 381 382 384 385 387 388 390 391 393 394 396 397 399 400 402	<210 <211 <212 <213 <400 Met 1 Val Asp Val Lys 65 Glu	> Si > Li > Ti > Oi > Si Ser Gly Val Asn 50 Lys Tyr	EQ II ENGTI YPE: RGANI EQUEI Val Phe Ile 35 Ala Asp Ala His Ser	PRT ISM: ISM: ICE: Gln Lys 20 Ser Ala Pro Gln Ser 100	Bacs 15 Ala 5 Glu Ala Ser Ser 85 Gln	Ala Thr Lys Ala Val 70 Val Gly	Gly Met Gly Thr 55 Ala Pro	Lys Ser Gly 40 Leu Tyr Tyr Thr	Ser Ala 25 Lys Asp Val Gly Gly 105	Ser 10 Met Val Glu Glu Ile 90 Ser	Thr Ser Gln Lys Glu 75 Ser Asn	Glu Ser Lys Ala 60 Asp Gln Val	Lys Ala Gln 45 Val His Ile Lys Asn	Lys Lys 30 Phe Lys Ile Lys Val 110	Tyr 15 Lys Glu Ala Ala 95 Ala	Lys Tyr Leu His 80 Pro	1074
369 371 373 375 381 382 384 385 387 388 391 393 394 400 402 403	<210 <211 <212 <213 <400 Met 1 Val Asp Val Lys 65 Glu Ala Ile	O> SI > LI P> TY S> OI O> SI Ser Gly Val Asn 50 Lys Tyr Leu Asp	EQ II ENGTI YPE: RGANI EQUEI Val Phe Ile 35 Ala Asp Ala His Ser	D NO: H: 35 PRT ISM: NCE: Gln Lys 20 Ser Ala Pro Gln Ser 100 Gly	Bacc 15 Ala 5 Gln Glu Ala Ser 85 Gln Ile	Ala Thr Lys Ala Val 70 Val Gly Asp	Gly Met Gly Thr 55 Ala Pro Tyr Ser	Lys Ser Gly 40 Leu Tyr Tyr Thr Ser 120	Ser Ala 25 Lys Asp Val Gly Gly 105 His	Ser 10 Met Val Glu Glu Ile 90 Ser	Thr Ser Gln Lys Glu 75 Ser Asn	Glu Ser Lys Ala 60 Asp Gln Val Leu	Lys Ala Gln 45 Val His Ile Lys Asn 125	Lys 30 Phe Lys 11e Lys Val 110 Val	Tyr 15 Lys Glu Ala Ala 95 Ala	Lys Tyr Leu His 80 Pro Val Gly	1074
369 371 373 375 381 382 384 385 387 388 390 391 393 394 400 402 403 405	<210 <211 <212 <213 <400 Met 1 Val Asp Val Lys 65 Glu Ala Ile Gly	O> SI > LI P> TY S> OI O> SI Ser Gly Val Asn 50 Lys Tyr Leu Asp	EQ II ENGTI YPE: RGANI EQUEI Val Phe Ile 35 Ala Asp Ala His Ser	D NO: H: 35 PRT ISM: NCE: Gln Lys 20 Ser Ala Pro Gln Ser 100 Gly	Bacc 15 Ala 5 Gln Glu Ala Ser 85 Gln Ile	Ala Thr Lys Ala Val 70 Val Gly Asp	Gly Met Gly Thr 55 Ala Pro Tyr Ser	Lys Ser Gly 40 Leu Tyr Tyr Thr Ser 120	Ser Ala 25 Lys Asp Val Gly Gly 105 His	Ser 10 Met Val Glu Glu Ile 90 Ser	Thr Ser Gln Lys Glu 75 Ser Asn	Glu Ser Lys Ala 60 Asp Gln Val Leu Tyr	Lys Ala Gln 45 Val His Ile Lys Asn 125	Lys 30 Phe Lys 11e Lys Val 110 Val	Tyr 15 Lys Glu Ala Ala 95 Ala	Lys Tyr Leu His 80 Pro Val Gly	1074
369 371 373 375 381 382 384 385 387 388 390 391 393 400 402 403 405 406	<210 <211 <212 <213 <400 Met 1 Val Asp Val Lys 65 Glu Ala Ile Gly	O> SI > LI > TY S> OI O> SI Ser Gly Val Asn 50 Lys Tyr Leu Asp Ala 130	EQ II ENGTI YPE: RGAN: EQUEI Val Phe Ile 35 Ala Asp Ala His Ser 115 Ser	PRT ISM: ISM: ISM: ISM: ISM: ISM: ISM: ISM:	Bacca 15 Ala 5 Gln Glu Ala Ser 85 Gln Ile Val	Ala Thr Lys Ala Val 70 Val Gly Asp	Gly Met Gly Thr 55 Ala Pro Tyr Ser Ser	Lys Ser Gly 40 Leu Tyr Tyr Thr Ser 120 Glu	Ser Ala 25 Lys Asp Val Gly Gly 105 His	Ser 10 Met Val Glu Glu Ile 90 Ser Pro	Thr Ser Gln Lys Glu 75 Ser Asn Asp	Glu Ser Lys Ala 60 Asp Gln Val Leu Tyr 140	Lys Ala Gln 45 Val His Ile Lys Asn 125 Gln	Lys 30 Phe Lys 11e Lys Val 110 Val Asp	Tyr 15 Lys Glu Ala Ala 95 Ala Arg	Lys Tyr Leu His 80 Pro Val Gly Ser	1074

RAW SEQUENCE LISTING DATE: 08/28/2001 PATENT APPLICATION: US/09/837,235 TIME: 10:22:38

Input Set : A:\9725-005-999.txt

Output Set: N:\CRF3\08282001\I837235.raw

409	145					150					155					160
411	Ile	Gly	Val	Leu	Gly	Val	Ser	Pro	Ser	Ala	Ser	Leu	Tyr	Ala	Val	Lys
412		_			165					170					175	_
414	Val	Leu	Asp	Ser	Thr	Gly	Ser	Gly	Gln	Tyr	Ser	Trp	Ile	Ile	Asn	Gly
415			-	180		-		_	185	_				190		
417	Ile	Glu	Trp	Ala	Ile	Ser	Asn	Asn	Met	Asp	Val	Ile	Asn	Met	Ser	Leu
418			195					200		-			205			
420	Gly	Gly	Pro	Thr	Gly	Ser	Thr	Ala	Leu	Lys	Thr	Val	Val	Asp	Lys	Ala
421	-	210			-		215			-		220		_	_	
	Val	Ser	Ser	Gly	Ile	Val	Val	Ala	Ala	Ala	Ala	Gly	Asn	Glu	Gly	Ser
	225			-		230					235					240
426	Ser	Gly	Ser	Thr	Ser	Thr	Val	Gly	Tyr	Pro	Ala	Lys	Tyr	Pro	Ser	Thr
427		-			245			_	_	250		_	_		255	
429	Ile	Ala	Val	Glý	Ala	Val	Asn	Ser	Ser	Asn	Gln	Arg	Ala	Ser	Phe	Ser
430				260					265					270		
432	Ser	Ala	Gly	Ser	Glu	Leu	Asp	Val	Met	Ala	Pro	Gly	Val	Ser	Ile	Gln
433			275				-	280					285			
435	Ser	Thr	Leu	Pro	Gly	Gly	Thr	Tyr	Gly	Ala	Tyr	Asn	Gly	Thr	Ser	Met
436		290					295					300				
438	Ala	Thr	Pro	His	Val	Ala	Gly	Ala	Ala	Ala	Leu	Ile	Leu	Ser	Lys	His
439	305					310					315					320
441	Pro	Thr	Trp	Thr	Asn	Ala	${\tt Gln}$	Val	Arg	Asp	Arg	Leu	Glu	Ser	Thr	Ala
442					325					330					335	
444	Thr	Tyr	Leu	Gly	Asn	Ser	Phe	Tyr	Tyr	Gly	Lys	Gly	Leu	Ile	Asn	Val
				340					345					350		
445				340					343					330		
-	Gln	Ala	Ala	Ala	Gln				343					330		
-	Gln	Ala	Ala 355		Gln									330		
447 448		•	355											330		
447 448 450	<210)> SI	355 EQ II	Ala	: 16									330		
447 448 450 452	<210)> SI l> LI	355 EQ II ENGTI	Ala D NO H: 20	: 16	÷							,	330		
447 448 450 452 454	<210 <211 <212)> SI l> LI 2> TY	355 EQ II ENGTI YPE:	Ala D NO H: 20	: 16 59	illus	s sul	otili	•				,	330		
447 448 450 452 454 456 460	<210 <211 <211 <213 <400	0> SI 1> LI 2> TY 3> OI 0> SI	355 EQ II ENGTI YPE: RGANI EQUEI	Ala NO H: 20 PRT ISM:	: 16 59 Baci 16				is				·			
447 448 450 452 454 456 460	<210 <211 <211 <213 <400	0> SI 1> LI 2> TY 3> OI 0> SI	355 EQ II ENGTI YPE: RGANI EQUEI	Ala D NO H: 20 PRT ISM:	: 16 59 Baci 16				is	Arg	Val	Gln	Ala		Ala	Ala
447 448 450 452 454 456 460 462 463	<210 <211 <211 <213 <400 Ala	0> SI l> LI 2> TY 3> OI 0> SI Gln	355 EQ II ENGTI YPE: RGANI EQUEN	Ala D NO H: 20 PRT ISM: NCE: Val	: 16 59 Bac: 16 Pro 5	Trp	Gly	Ile	is Ser	10				Pro	15	
447 448 450 452 454 456 460 462 463 465	<210 <211 <211 <213 <400 Ala	0> SI l> LI 2> TY 3> OI 0> SI Gln	355 EQ II ENGTI YPE: RGANI EQUEN	Ala O NO H: 20 PRT ISM: NCE: Val	: 16 59 Bac: 16 Pro 5	Trp	Gly	Ile	is Ser Gly	10				Pro Val	15	
447 448 450 452 454 456 460 462 463 465 466	<210 <211 <211 <211 <400 Ala 1 His)> SI 1> LI 2> TY 3> OI 3> SI Gln	355 EQ II ENGTI YPE: RGANI EQUEN Ser Arg	Ala O NO H: 20 PRT ISM: NCE: Val Gly 20	: 16 59 Bac: 16 Pro 5 Leu	Trp Thr	Gly Gly	Ile Ser	is Ser Gly 25	10 Val	Lys	Val	Ala	Pro Val 30	15 Leu	Asp
447 448 450 452 454 460 462 463 465 466 468	<210 <211 <211 <211 <400 Ala 1 His)> SI 1> LI 2> TY 3> OI 3> SI Gln	355 EQ II ENGTH YPE: RGANI EQUEN Ser Arg	Ala O NO H: 20 PRT ISM: NCE: Val	: 16 59 Bac: 16 Pro 5 Leu	Trp Thr	Gly Gly	Ile Ser Asp	is Ser Gly 25	10 Val	Lys	Val	Ala Gly	Pro Val 30	15 Leu	Asp
447 448 450 452 454 456 460 462 463 465 466 468 469	<210 <211 <213 <400 Ala 1 His	0> Si 1> Li 2> TY 3> OI 0> Si Gln Asn	355 EQ II ENGTH YPE: RGANI EQUEN Ser Arg Ile 35	Ala O NO H: 20 PRT ISM: NCE: Val Gly 20 Ser	: 16 69 Bac: 16 Pro 5 Leu	Trp Thr His	Gly Gly Pro	Ile Ser Asp	is Ser Gly 25 Leu	10 Val Asn	Lys Ile	Val Arg	Ala Gly 45	Pro Val 30 Gly	15 Leu Ala	Asp Ser
447 448 450 452 454 456 460 462 463 466 468 469 471	<210 <211 <211 <213 <400 Ala 1 His	O> SI 1> LI 2> TY 3> OI O> SI Gln Asn Gly	355 EQ II ENGTH YPE: RGANI EQUEN Ser Arg Ile 35 Pro	Ala O NO H: 20 PRT ISM: NCE: Val Gly 20 Ser Gly	: 16 59 Bac: 16 Pro 5 Leu Thr	Trp Thr His	Gly Gly Pro Ser	Ile Ser Asp 40 Thr	is Ser Gly 25 Leu Gln	10 Val Asn Asp	Lys Ile Gly	Val Arg Asn	Ala Gly 45 Gly	Pro Val 30 Gly	15 Leu Ala	Asp Ser
447 448 450 452 454 466 463 465 466 468 469 471 472	<210 <211 <211 <400 Ala 1 His Thr	0> SI 1> LI 2> TY 3> OI 0> SI Gln Asn Gly Val 50	355 EQ II ENGTH YPE: RGANI EQUEN Ser Arg Ile 35 Pro	Ala O NO H: 20 PRT ISM: NCE: Val Gly 20 Ser Gly	Baci 16 Pro 5 Leu Thr	Trp Thr His Pro	Gly Gly Pro Ser 55	Ile Ser Asp 40 Thr	is Ser Gly 25 Leu Gln	10 Val Asn Asp	Lys Ile Gly	Val Arg Asn 60	Ala Gly 45 Gly	Pro Val 30 Gly His	15 Leu Ala Gly	Asp Ser Thr
447 448 450 452 454 456 460 462 463 465 466 468 471 472 474	<210 <211 <211 <211 <400 Ala 1 His Thr	0> SI 1> LI 2> TY 3> OI 0> SI Gln Asn Gly Val 50	355 EQ II ENGTH YPE: RGANI EQUEN Ser Arg Ile 35 Pro	Ala O NO H: 20 PRT ISM: NCE: Val Gly 20 Ser Gly	Baci 16 Pro 5 Leu Thr	Trp Thr His Pro	Gly Gly Pro Ser 55	Ile Ser Asp 40 Thr	is Ser Gly 25 Leu Gln	10 Val Asn Asp	Lys Ile Gly Asn	Val Arg Asn 60	Ala Gly 45 Gly	Pro Val 30 Gly His	15 Leu Ala Gly	Asp Ser Thr
447 448 450 452 454 456 460 462 463 465 466 468 471 472 474 475	<210 <211 <211 <400 Ala 1 His Thr Phe	O> SI 1> LH 2> TY 3> OI O> SI Gln Asn Gly Val 50 Val	355 EQ II ENGTH YPE: RGANI EQUEN Ser Arg Ile 35 Pro	Ala D NO H: 20 PRT ISM: NCE: Val Gly 20 Ser Gly Gly	: 16 59 Bac: 16 Pro 5 Leu Thr Glu	Trp Thr His Pro Ile 70	Gly Gly Pro Ser 55 Ala	Ile Ser Asp 40 Thr	is Ser Gly 25 Leu Gln Leu	10 Val Asn Asp	Lys Ile Gly Asn 75	Val Arg Asn 60 Ser	Ala Gly 45 Gly Ile	Pro Val 30 Gly His	15 Leu Ala Gly Val	Asp Ser Thr Leu 80
447 448 450 452 454 460 462 463 465 466 468 471 472 474 475 477	<210 <211 <211 <400 Ala 1 His Thr Phe	O> SI 1> LH 2> TY 3> OI O> SI Gln Asn Gly Val 50 Val	355 EQ II ENGTH YPE: RGANI EQUEN Ser Arg Ile 35 Pro	Ala O NO H: 20 PRT ISM: NCE: Val Gly 20 Ser Gly	: 16 59 Bac: 16 Pro 5 Leu Thr Glu Thr	Trp Thr His Pro Ile 70	Gly Gly Pro Ser 55 Ala	Ile Ser Asp 40 Thr	is Ser Gly 25 Leu Gln Leu	10 Val Asn Asp Asn	Lys Ile Gly Asn 75	Val Arg Asn 60 Ser	Ala Gly 45 Gly Ile	Pro Val 30 Gly His	15 Leu Ala Gly Val Gly	Asp Ser Thr Leu 80
447 448 450 452 454 460 462 463 465 466 468 471 472 474 475 477	<210 <211 <211 <400 Ala 1 His Thr Phe His 65 Gly	O> SI 1> LI 2> TY 3> OI O> SI Gln Asn Gly Val 50 Val	355 EQ II ENGTH YPE: RGAN: EQUEN Ser Arg Ile 35 Pro Ala Ala	Ala O NO H: 20 PRT ISM: NCE: Val Gly 20 Ser Gly Gly Pro	Baci 16 Pro 5 Leu Thr Glu Thr	Trp Thr His Pro Ile 70 Ala	Gly Gly Pro Ser 55 Ala Glu	Ile Ser Asp 40 Thr Ala Leu	is Ser Gly 25 Leu Gln Leu	10 Val Asn Asp Asn Ala 90	Lys Ile Gly Asn 75 Val	Val Arg Asn 60 Ser Lys	Ala Gly 45 Gly Ile Val	Pro Val 30 Gly His Gly Leu	15 Leu Ala Gly Val Gly 95	Asp Ser Thr Leu 80 Ala
447 448 450 452 454 460 462 463 465 466 468 471 472 474 475 477 478	<210 <211 <211 <400 Ala 1 His Thr Phe His 65 Gly	O> SI 1> LI 2> TY 3> OI O> SI Gln Asn Gly Val 50 Val	355 EQ II ENGTH YPE: RGAN: EQUEN Ser Arg Ile 35 Pro Ala Ala	Ala D NO H: 20 PRT ISM: NCE: Val Gly 20 Ser Gly Gly Pro Gly	Baci 16 Pro 5 Leu Thr Glu Thr	Trp Thr His Pro Ile 70 Ala	Gly Gly Pro Ser 55 Ala Glu	Ile Ser Asp 40 Thr Ala Leu	is Ser Gly 25 Leu Gln Leu Tyr	10 Val Asn Asp Asn Ala 90 Ala	Lys Ile Gly Asn 75 Val	Val Arg Asn 60 Ser Lys	Ala Gly 45 Gly Ile Val	Pro Val 30 Gly His Gly Leu Glu	15 Leu Ala Gly Val Gly 95	Asp Ser Thr Leu 80 Ala
447 448 450 452 454 456 460 462 463 465 466 471 477 477 478 480 481	<210 <211 <211 <400 Ala 1 His Thr Phe His 65 Gly Ser	O> SI l> LI 2> TY 3> OI O> SI Gln Asn Gly Val Val Val	355 EQ II ENGTH YPE: RGANI EQUEN Ser Arg Ile 35 Pro Ala Ala Ser	Ala D NO H: 20 PRT ISM: NCE: Val Gly 20 Ser Gly Gly Pro Gly 100	Bac: 16 Pro 5 Leu Thr Glu Thr Asn 85 Ser	Trp Thr His Pro Ile 70 Ala Val	Gly Gly Pro Ser 55 Ala Glu Ser	Ile Ser Asp 40 Thr Ala Leu Ser	is Ser Gly 25 Leu Gln Leu Tyr Ile 105	10 Val Asn Asp Asn Ala 90 Ala	Lys Ile Gly Asn 75 Val	Val Arg Asn 60 Ser Lys Gly	Ala Gly 45 Gly Ile Val Leu	Pro Val 30 Gly His Gly Leu Glu 110	15 Leu Ala Gly Val Gly 95 Trp	Asp Ser Thr Leu 80 Ala
447 448 450 452 454 456 460 462 463 465 466 471 477 478 480 481 483	<210 <211 <211 <400 Ala 1 His Thr Phe His 65 Gly Ser	O> SI l> LI 2> TY 3> OI O> SI Gln Asn Gly Val Val Val	355 EQ II ENGTH YPE: RGANI SEQUEN Ser Arg Ile 35 Pro Ala Ala Ser Asn	Ala D NO H: 20 PRT ISM: NCE: Val Gly 20 Ser Gly Gly Pro Gly	Bac: 16 Pro 5 Leu Thr Glu Thr Asn 85 Ser	Trp Thr His Pro Ile 70 Ala Val	Gly Gly Pro Ser 55 Ala Glu Ser	Ile Ser Asp 40 Thr Ala Leu Ser Ala	is Ser Gly 25 Leu Gln Leu Tyr Ile 105	10 Val Asn Asp Asn Ala 90 Ala	Lys Ile Gly Asn 75 Val	Val Arg Asn 60 Ser Lys Gly	Ala Gly 45 Gly Ile Val Leu Gly	Pro Val 30 Gly His Gly Leu Glu 110	15 Leu Ala Gly Val Gly 95 Trp	Asp Ser Thr Leu 80 Ala
447 448 450 452 454 466 466 466 467 477 477 478 481 483 484	<210 <211 <211 <400 Ala 1 His Thr Phe His 65 Gly Ser Gly	O> SI l> LI 2> TY 3> OB O> SI Gln Asn Gly Val Val Val Gly Asn	355 EQ II ENGTH YPE: RGANI SEQUEN Ser Arg Ile 35 Pro Ala Ala Ser Asn 115	Ala D NO H: 20 PRT ISM: NCE: Val Gly 20 Ser Gly Gly Pro Gly 100	Bace 16 Pro 5 Leu Thr Glu Thr Asn 85 Ser	Trp Thr His Pro Ile 70 Ala Val His	Gly Gly Pro Ser 55 Ala Glu Ser Val	Ile Ser Asp 40 Thr Ala Leu Ser Ala 120	Ser Gly 25 Leu Gln Leu Tyr Ile 105 Asn	10 Val Asn Asp Asn Ala 90 Ala Leu	Lys Ile Gly Asn 75 Val Gln Ser	Val Arg Asn 60 Ser Lys Gly Leu	Ala Gly 45 Gly Ile Val Leu Gly 125	Pro Val 30 Gly His Gly Leu Glu 110 Ser	15 Leu Ala Gly Val Gly 95 Trp	Asp Ser Thr Leu 80 Ala Ala Ser

VERIFICATION SUMMARY

DATE: 08/28/2001

PATENT APPLICATION: US/09/837,235

TIME: 10:22:39

Input Set : A:\9725-005-999.txt

Output Set: N:\CRF3\08282001\I837235.raw